

PGN1

TaqI

1 GTCGAGGCAGTCACTAACATGAAGTTTGACGAGGAGCCCACTATGGGAAGCTTATTCTCTTTTCGAT 69

HindIII

AluI

TaqI

50

SacI

AluI

HhaI XbaI

70 ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAAATTGATGGAGCTCTAAAGGTTGCTGGCTGT 138

89

119

121

NdeI

139 TTTCTTGTTCATATGATTAACCTCTAAACTTGTGTATAAATATTCTCTGAAAGTGCTTCTTTTGGCATA 207

150

206

NdeI

208 TGTAGGTTGGGCAAAAACGAGGAGATTGCTTCTCAATTGGAAGATGATGAACAGCCGAAGAAGAAA 276

Sau3AI

DdeI

277 TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAACGGTCGTGCTCCATGAACAGAGGT 345

309

305

FIG. 1A

*cancel
per
paper
#14*

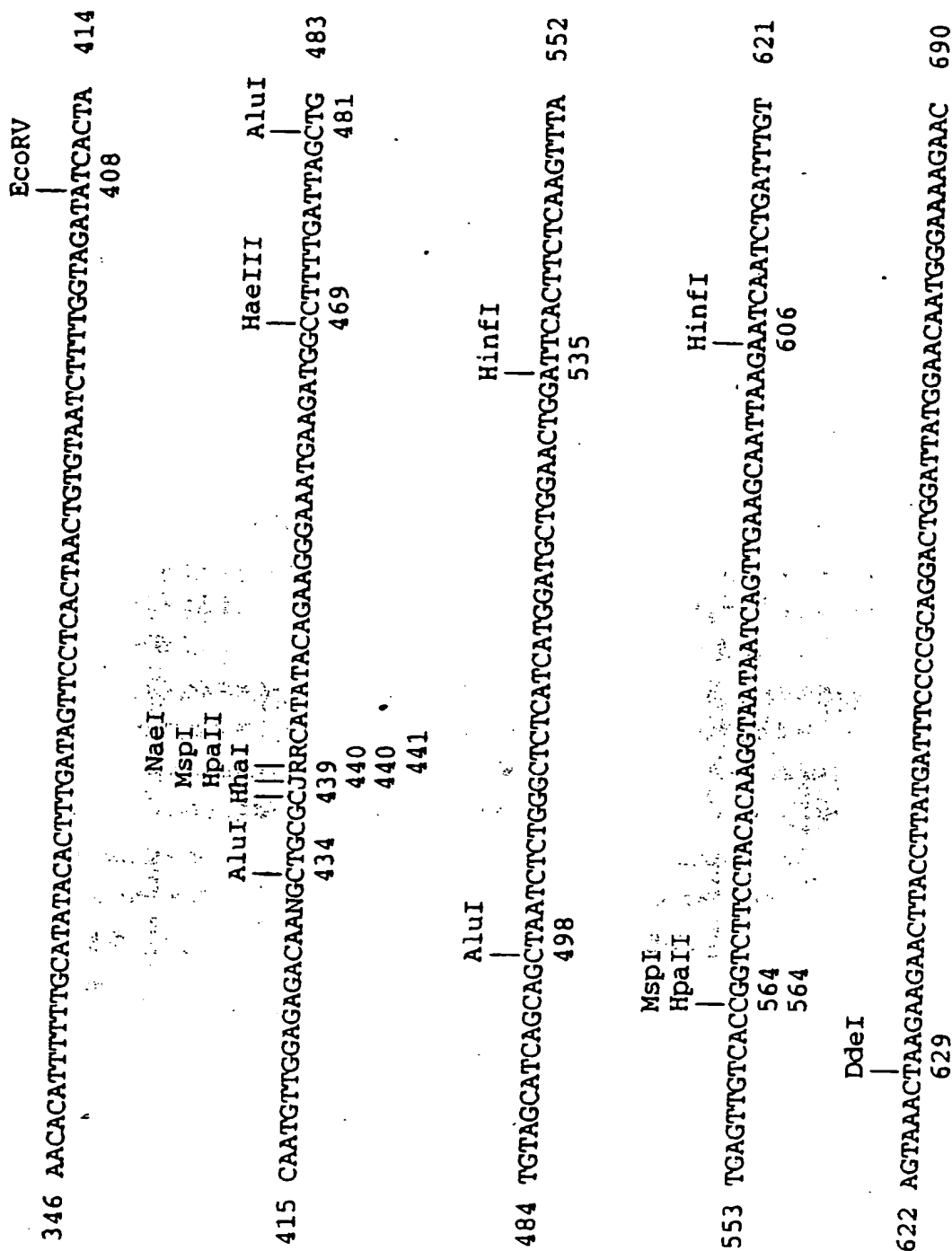


FIG. 1B

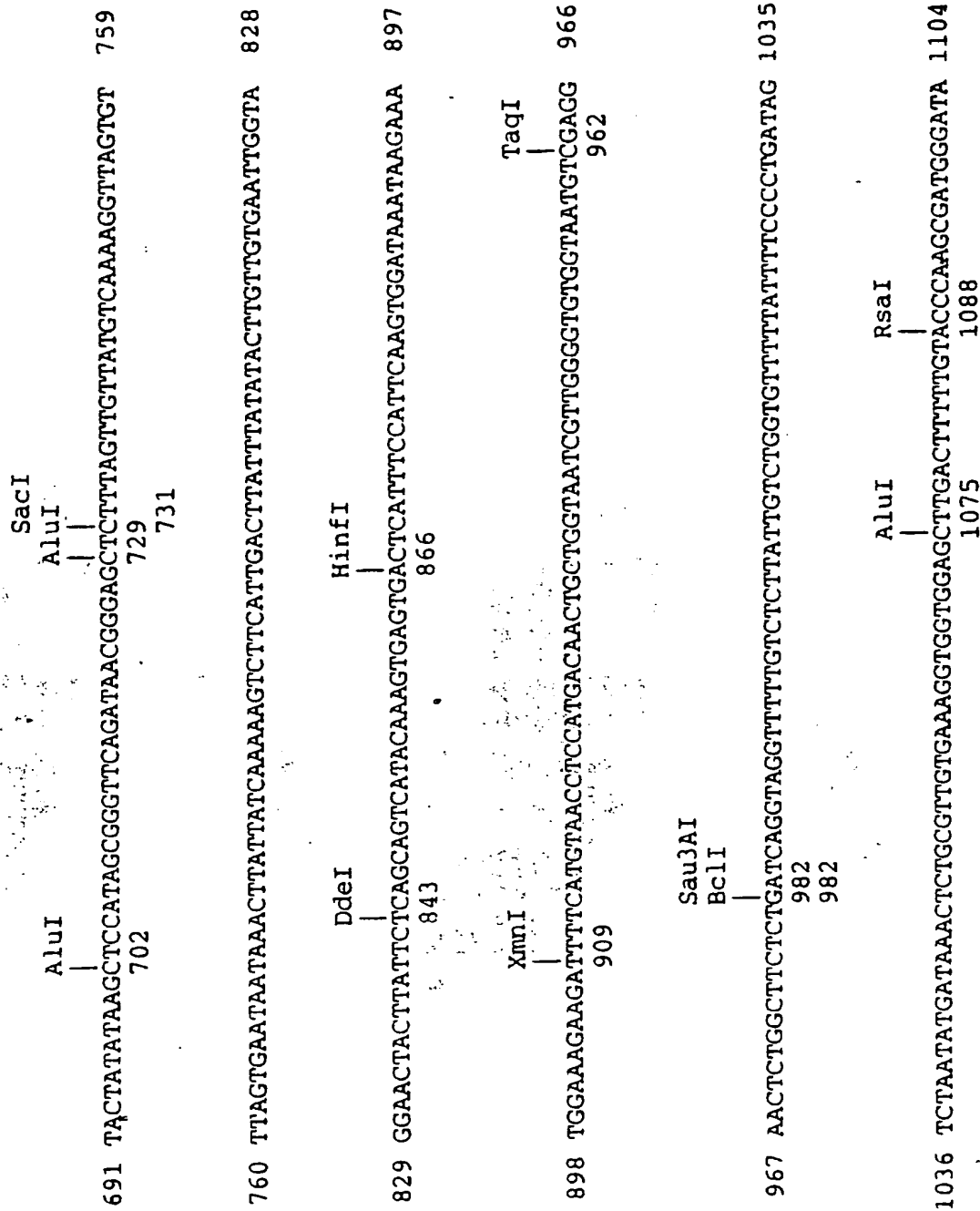


FIG. 1C

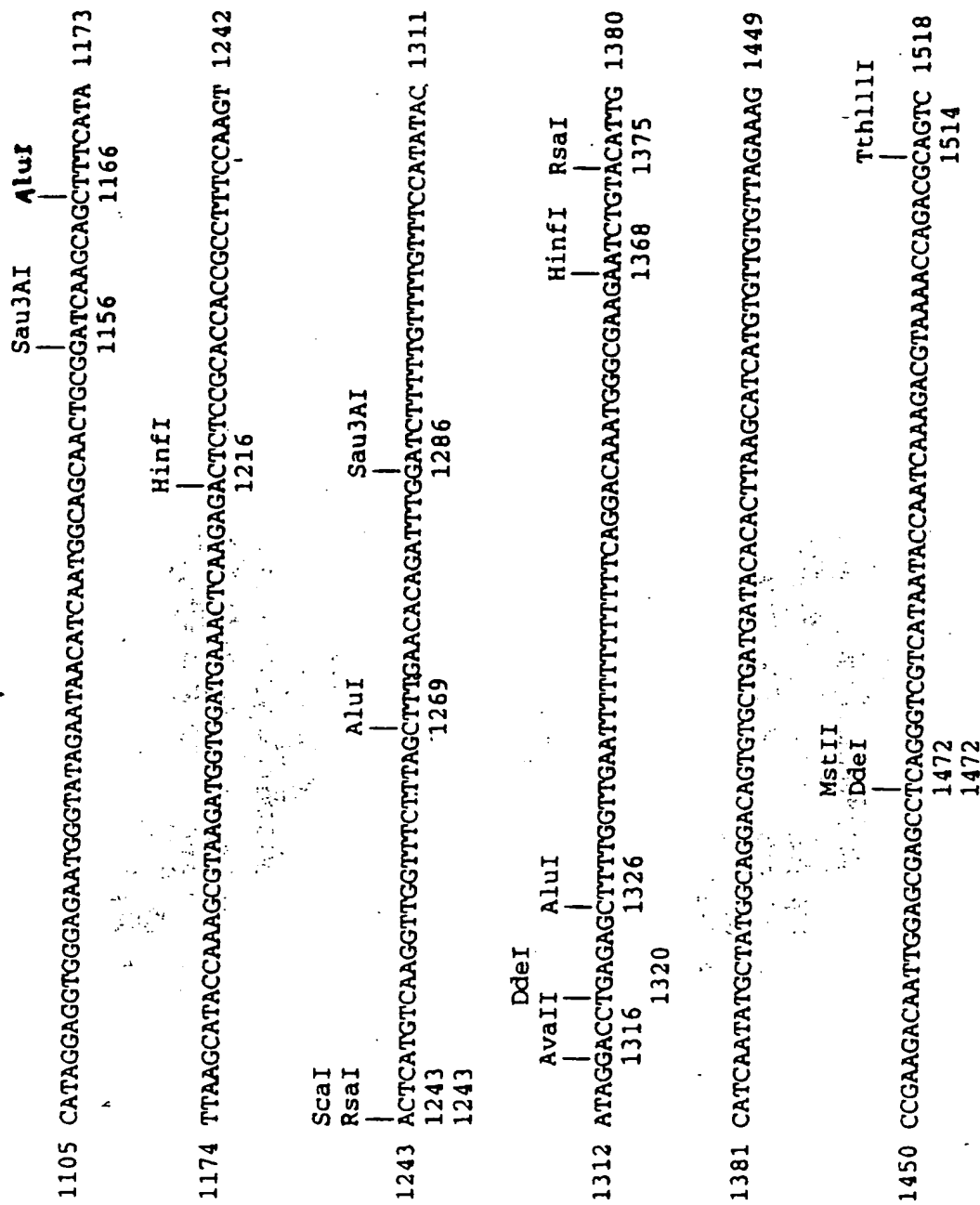


FIG. 1D

1519 TCTTTGGTTGAATGTGATGAAAGGGATGTGTCTTGGTATGTATGTACGAGTAACAAAAGAGAAGATGCA 1587
RsaI | 1564

1588 ATTGAGTAGTAGAAGATTGAGAGCTTTTTTAAAGCCCTTCAAGTGTGTGCTTTTATCTTATTGATATC 1656
AluI | DraI | EcoRV |
1613 1619 1654

1657 ATCCATTTCGCTTGTATTAATGCGTCTTTAGATATGTTTCTGTCTTCTCAGTGTCTGAATATCTGAT 1725
DdeI | 1706

1726 AAGTGCAATGTGAGAAAGCCACACCAACCAAAATATTCAAATCTTATATTTTAAATAATGTGGAATCA 1794
TaqI | HinfI |
1790 1788

1795 CTCGGAGTTGCCACCTTCTGTGCCAATTGTGCTGAATCTATCACACTAAAAAACAATTTCTTCAAGGT 1863
HinfI | 1829

1864 AATGACTTGTGGACTATGTTCTGAATTTCTCATTAAGTTTTTATATTTTTTGAAGTTTAAAGTTTTTACCTTC 1932
EcoRI | 1887

FIG. 1E

FIG. 1F.

NCG-186 Linear

LENGTH = 4325

**Xhol
Taqi
Avai**

1 CTCGAGGCAGTCACCTAACATGAAGTTTGACGAGGAGCCCACTATGGGAGCTTATTTCCTTTTCGAT
 2 3 2
 2 3 2
 50 52 66 69
 Aval HindIII AclI TgaI

70 ACTCTAATTGAGCCGTGGCTCTATCTAGACCAATTAGAAATTGATGGAGCTCTAAAGGTTGCTGGCTGT 138

HhaI XbaI SacI
| | |
A101 | |

89 95 119 121

139 TTCTTGTCATATGATTAACTTCTAAACTTGTGTATAAATATTCCTGAAAGTGCTTCCTTTTGCAATA 207
NdeI NdeI
150 121

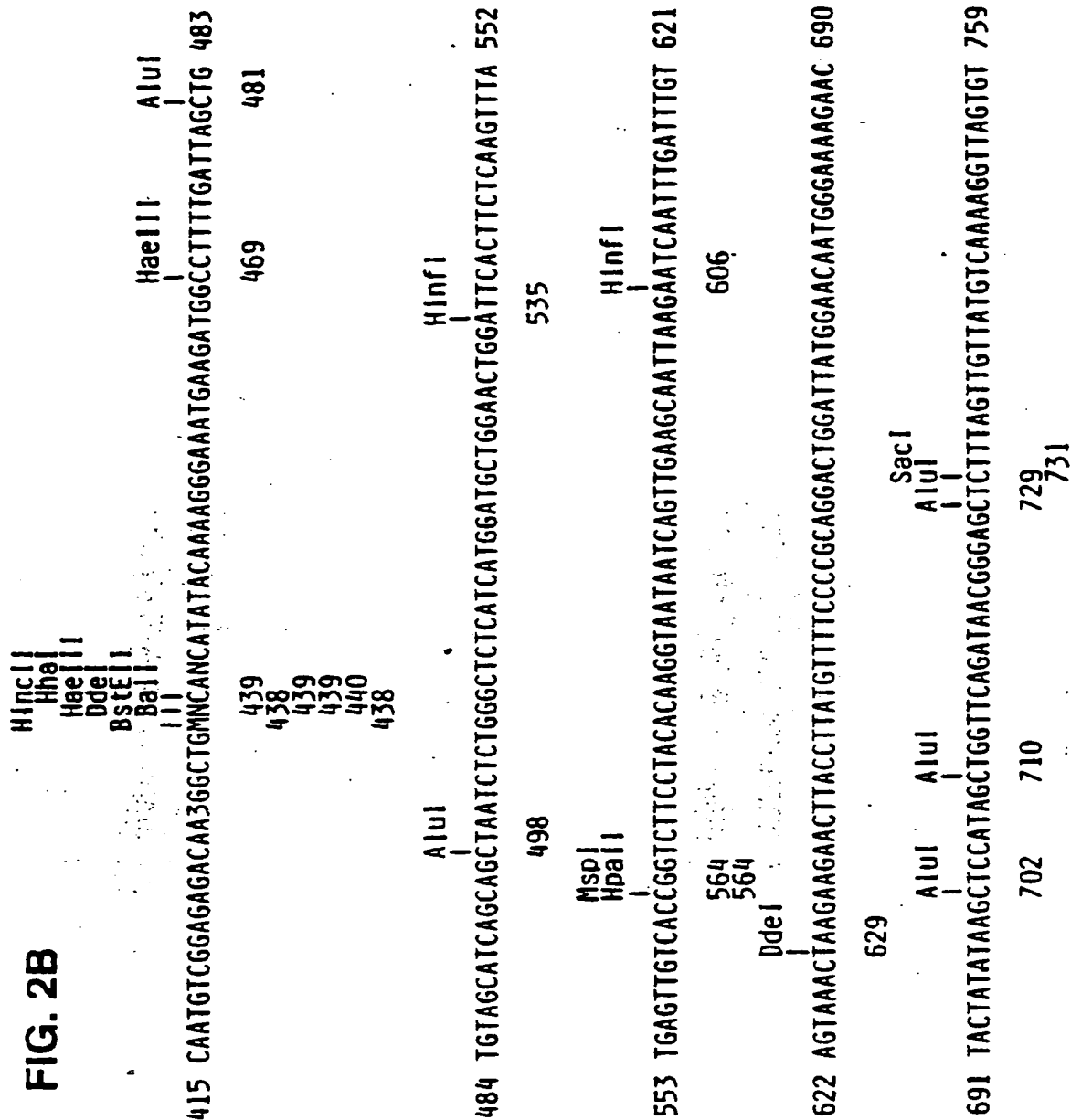
208 TGTAGGTTGGGCAAAACGAGGAAGATTGCTTCTCAATTGGAGAGGATGAACAGCCGAGAGAGAAA 206
275

277 TAAGAATAGGCAGTCTCTGCTACTCAATGGATCCTCAGTCTATAACGGTCGTGCTCCCAATGAACAGAGGT 345

346 AAACATTTTTTGCATATACACTTTTGAAAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA
EcoRV
414

FIG. 2A

FIG. 2B



760 TTAGTGAATAATAACTTATACCACAAGCTTCATTGACTTATTTATATATACTTGTGTGTAATGGCTAG 828
DdeI HinfI
829 GAAC TACTATTCTCAGCAGTCATACAAAGTGAGTGACTCATTTCCGTTCAAGTGGGATAAATAAGAAAT 897
842 865
XmnI
908 961
967 ACTCTGGCTCTCTGATCAGGTAGGTTTTTGTGCTCTTATTTGCTGGTGTATTTTATTTCCCTGATAGT 1035
981 981
1036 CTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTGACTTTTTGTACCCAAAGCGATGGGATAC 1104
AluI RsaI
1074 1087
1105 ATAGGAGGTGGGAGAAATGGGTATAGATAAATAACATCAATGGCAGCAACTGGCGATCAAGCAGCTTTCATAT 1173
Sau3AI AluI
1155 1165
1174 TANGCATACCAAAGCGTAGATGGTGGATGAANCTCAGAGAGCTCTCCGCCACCACCGCCTTTCCAAGTA 1242
HinfI ScaI RsaI
1215 1242

FIG. 2C

1243 CTATGTC AAGGTTGGTTTCCTTTAGCTTTGAACACAGATTGGATCTTTTGGTTTGGTTTCCATATACT 1311
AluI | Sau3AI |
1268 1285 1311

1312 TAGGACCTGAGAGCTTTTGGTTGATTTTTTTTCAGGACAAATGGGCGAAGATCTGTACATTGCAICA 1380
Ddel | AalI | AluI | HinfI | RsaI |
1315 1325 1363 1370

1381 ATATGCTATGGCAGGACAGTGTGCTGATACACACTTAAGCATCATGTGGAAAGCCAAAGACAATTGGAG 1449
HinfI | Ddel |
1456 1454

1450 CGAGACTCAGGGTGTGTCATAATACCAATCAAAGACGTAAACCAGCGCAACCTCTTTGGTTGAATGTA 1518
RsaI |
1548

1519 ATGAAAGGGATGTGCTCTTGGTATGTATGTACGAATAACAAAGAGAGAGATGGGAATTAGTAGAGAAATA 1587
AluI | EcoRV |
1596 1635

1588 TTTGGGAGCTTTTAAAGCCCTTCAAGTGTGCTTTTATCTTATTGATATCATCCATTTCGGTTGTTAA 1656
XbaI | Ddel |
1664 1687

1657 TCGGTCTCTAGATATGTTCCCTATATCTTTCTCAGTGTCTGTATAAGTGAAATGTGAGAAAMCCATACCAA 1725

1657 TGGGTCTCTAGATATGTTCCCTATATCTTTCTCAGTGTCTGATAGTGAATGTGAGAAACCATACCA 1725

1726 ACCAAATATTCAAATCTTATTTTAAATAATGTTGAATCAGTCGGAGTTGCCACCTTCGTGCGCAATTG 1794
HinfI |
1761

1795 TGTGAACTATCAGACTAGAAAAAACATTCTTCAAGGTAATGACTTGTGGACTAATGTTCTCAGAATTC 1863
HinfI |
EcoRI |
1800 1859

1864 TCATTAAGTTTTTATTTTCTCGAAGTTTAAGTTTTTACCTTCGTGTTTTGAATATATCGTTTCATAAGATG 1932
BstNI | AluI | SphI | Sau3AI |
1933 TCACGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTGTGCACACACCTTCAA 2001
1940 1950 1973 1971

2002 CACCTAAGAGCTTCTCTCTCACAGCGCACACACATATGCATGCAATATTTACAGTGATCGCCATGCAA 2070
DdeI | AluI | HhaI | NdeI | SphI | Sau3AI |
2006 2012 2028 2036 2042 2058 2044

2071 ATCTCCATTCTCACCCTATAAATTAGAGCCTCGGCTTCACCTCTTACTCAAACCAAACTCATCCTAC 2139
AluI |

2140 GAACATACACAAATGGCGAACAAGCTCTTCCTCGTCTGGCAACTCTCGCCTTGTCTTCCTTCACCC 2208
METATAasnLysLeuPheLeuValSerAlaThrLeuAlaLeuPheLeuLeuThr
2164

2140 GAACATACACAAATGGCGAACAGCTCTTCCTCGTCTGGCAACTCTCGCCTTGTCTTCCTTCACACC 2208
 METAlAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPhePheLeuLeuThr
 2164

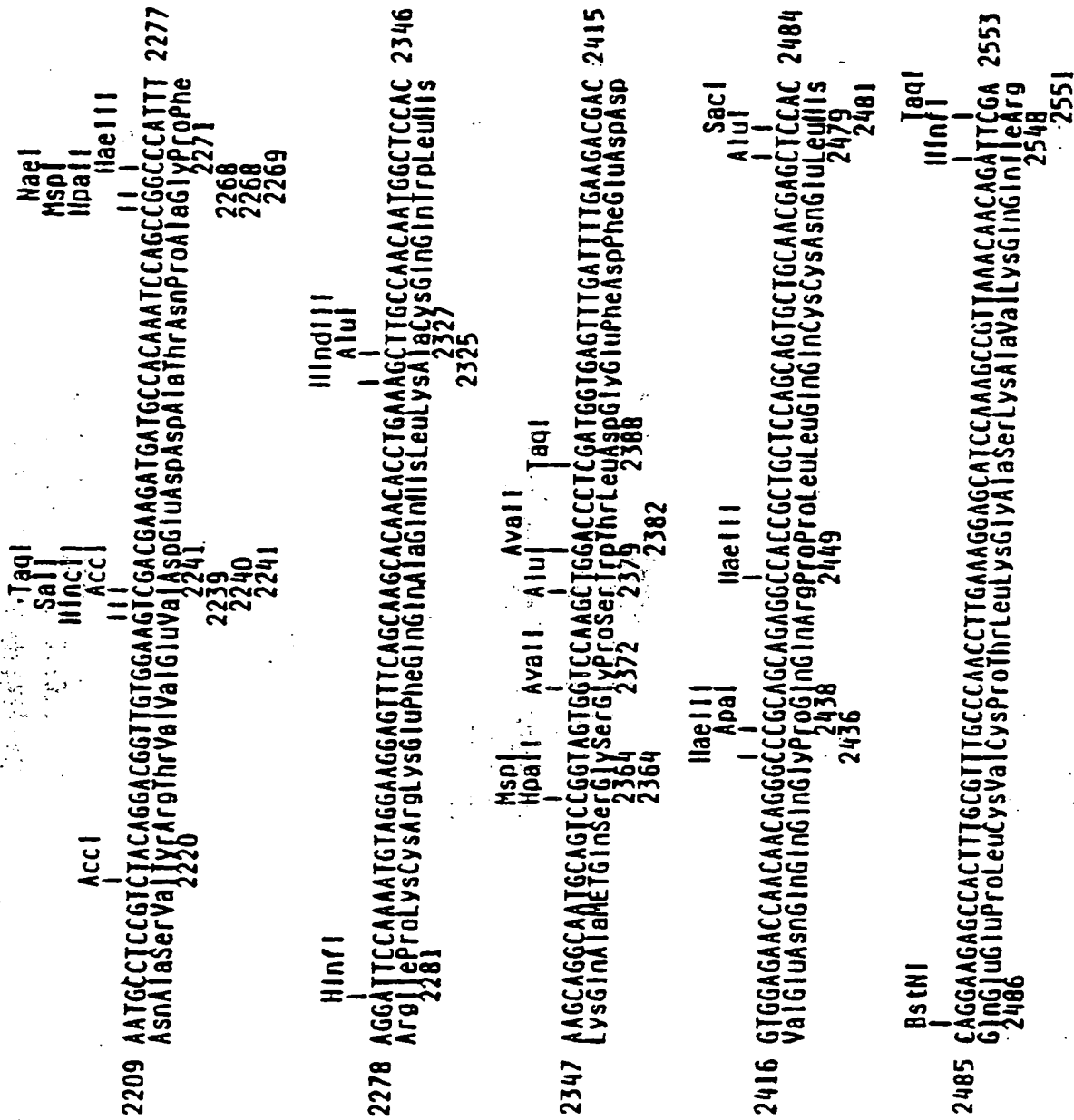


FIG. 2F

[illegible]2954
2954

2968 CAATGACAGATTTTCTTTTCTAATGCTAATTAAGCCTTCAAGGCTAGTATGATAAAAGATCATCCA 3036
Sau3AI

3028

3037 ATGGGATCCCAACAAGACATCAAACTGGTTTGATCAGATACTTCAAACTATTTTGGTATTCATTAAA 3105
Sau3AI
HinfI

3041 3053 3069 3069
3041

HinfI

3016 TTATGCAAGTGTCTTTTATTTGGTGAAGACTCTTTAGAGCAAGACGACAGCAGTAATAAANA 3174
3135

3175 ACAAGTTCAGTTTAAAGATTGGTTATGACTTATTGTCATTGTAATAATAGTATGATTAATA 3243
3244 GTTTTATTATATAATGCTTGTCTATTCAGATTGAGAACATTAATATGATACTGTCCACATATCCA 3312

HdeI

3313 TATATTAAGTTTCATTCTGTTCAACATATGATAAGATGGTCAATGATTATGAGTTTGTATTATAC 3381
3341

3382 CTGAAGAAAGATAAGTGAAGCTTCGAGTTTCTGAAGGGTACGTGATCTTCATTCTTGGCTAAAGCGA 3450
TaqI
AluI
Sau3AI
RsaI
3402 3405 3421 3425

3451 ATATGACATCACCCTAGAGAAAGCCGATAATAGTAACTCTGTCTTGGTTTGGTTAATCAACCGA 3519
FIG. 2H

3520 ACCGGTAGCTGAGTGTCAAGTCAGCAACCATATGTCATTCGTTAGATTCCTGGTTTAA 3568

3589 GTTGTAAACCGGTATTTTCATTTGGTGAACACCTAGAGCCAGCCANECITTTTAATCTAATTTTGGCA 3657

3658 ACCGAGAGTCACCCACACCCTCTCCACTAAAGCCCTGAACCTTACTGAGAGAGAGCAGAGCAGNCANHAAGAA 3726

3727 CAAATAAACCCGAAGATGAGACCACCAACGTGCGGCGGGACGTTACGGGGACGGGGAGGAAGAGAATGR 3795

3796 CGGCGGSMHTTGGTGGCGGCGGCGGACGTTTGGTGGCGGCGGTGGACGTTTGGTGGCGGCGGTGGA 3864

3801 3804 3863

3865 C C T T G G G T G G A T A T C G T G A C C A G G A C C T C C C A G T G A G T C A T T G G T G G T T A C T C T T T C T A G 3933

ECORV AvalI Ddel

3880 3892 3930

3934 TCGAATCTATTCTTGGCTCGCTGGTTTACCGATAAAGCTTAAGACTTTATTGATAAAGTCTCA 4002
 3935
 4003 GCCTTGAATGTGAATGAACAGTCTTCTGCTTATTAGTGTCTTCTTTTGGAGTTGAATCAGTCTCA 4071
 4004
 4072 GCACCTTTGTAGATTCACTTTGTGTTTAAAGTTAAAGGTAGAAACTTTGTGACTTGTCTCCGTTATG 4140
 4141 ACAAGGTTAACTTTGTGTTTAAACAGAGTTGGACCTTCTCCATGCTTGTAGGGTGATGCTGTG 4209
 4210 GACCAAGCTCTCTCAGGCGAAGATCCTTACTTCAATGCCCAATCTACTTGGAAACAAGACACAGAT 4278
 4279 TGGGAAGTTGATGAGATCCAAAGCTTGGGCTGCAGGCTCAGCAATTC 4325
 4294 4302 4300
 4316 4321
 4314
 4315
 4316

4315
4316

Brassica campestris ACP Genomic Sequence

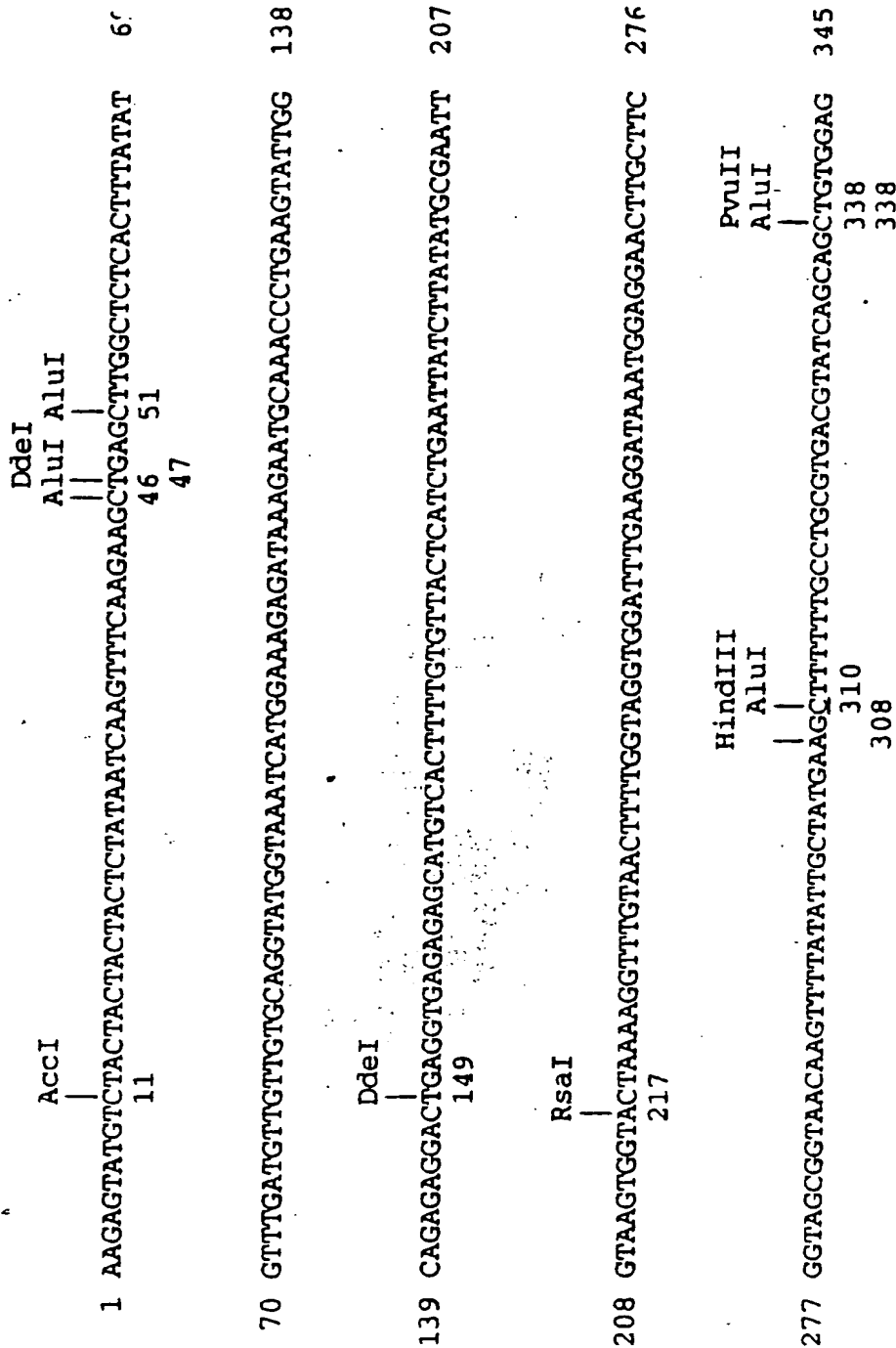


FIG. 3A

346 AAGATGGTATTAGAAAGGGCTTTTCACATTTTGTGTGTGACAAATATTAAATTCGGCCGGTATGGTTT 414
 MspI
 HpaII
 HaeIII
 ||
 403
 404
 404

 415 GGTAAAGACTTGTGAGAGACGTGTGGGGTTTTTTTGATGATAATTAGTCTGTGTTTAGAACGAACAA 483

 484 GACTTGTGNGTATGCTTTTTTTTAACTTGAGGGGGTTTGTGTGTAGTAGGAACCTTGACTTTGTCT 552
 Tth1111I
 |
 547

 553 CTTTCTCTCAAGATCTGATTTGGTAAGGTCTGGGTGGTAGTACTGTTTGGTTTAAATTGTTTGTGACTATT 621
 Sau3AI
 BglII
 |
 564
 564
 593
 593

 622 GAGTCACTGTGGCCCATTTGACTTTTAAATTAGGCTGGTATATTTTTTGGTTTAAACCGGCTCTGAGATAG 690
 HinfI
 |
 623
 634
 646
 HpaII
 DraI MspI DdeI
 |
 673 678 683
 678

FIG. 3B

691 701 715 699

TaqI
HinfI
DraI
691 T G C A A T T T C G A T T C A G T C A A T T T T A A A T T C T T C A A G G T A A T G G C T G A A T A C T T G T A T A G T T T T A A G A C 759
701
715
699

StuI
HaeIII
HaeIII
HindIII
AluI
760 T T A A C A G G C C T T A A A A G G C C C A T G T T A T C A T A A A C G T C A T T G T T A G A G T G C A C C A A G C T T A T A A A T 828
768
778
819
817

StuI
HaeIII
BstNI
StuI
HaeIII
HaeIII
829 G T A G C C A G G C C T T A A A A G A C T T A A C A G G C C T T A A A A G A C T T A A C A T T C C T T A A A A G G C C C A T G T T A T C A 897
835
857
857
838
838

AluI
StuI
HaeIII
BstNI
HaeIII
898 T A A A A C G T C A T C G T T T T G A G T G C A C C A A G C T A A A T G T A G C C A G G C C T T A A A A G A C T T A A C A G G C C T T A A 966
927
939
942
942
961
961

FIG. 3C

[illegible]

FIG. 3D

HincII		AluI	HinfI
1243	GTTAACTCTCCAGCGCATGTTTGATTATGTTGAGAAATAGAAAAAATGTTAGCTTTACGAATCTTTAG	1296	1303
1243			
Sau3AI		TaqI	
BclI		Sau3AI	
1312	TGATCATTTCAATTGGATTGTGCAATCTTGTGTGACATTGTGAGGCTTGTGTAGATTTCGATCTGTATTCA	1369	1380
1313		1368	
1313			
HinfI	AluI	DraI	
1381	TTTTGAATCACAGCTATAATAGTCATTTGAGTAGTAGTGTGTTTAAATGAACATGTTTGTGTATTGA	1425	1449
1386	1394		
AluI			
1450	TGGAACAAACAGGCAGCAACACGAGGATTAGTTTCCAGAGCCAGCTTTGGTTTCAACGACTAATCTC	1518	
	AlaAlaThrThrArgIleSerPheGlnLysProAlaLeuValSerThrThrAsnLeu	1496	
1519	TCCTTCAACCTCCGCCGTTCAATCCCACTCGTTTCTCAATCTCCTGGCGGTATGTTCTCATTCCTCAG	1587	
	SerPheAsnLeuArgArgSerIleProThrArgPheSerIleSerCysAla	1568	1584

FIG. 3E

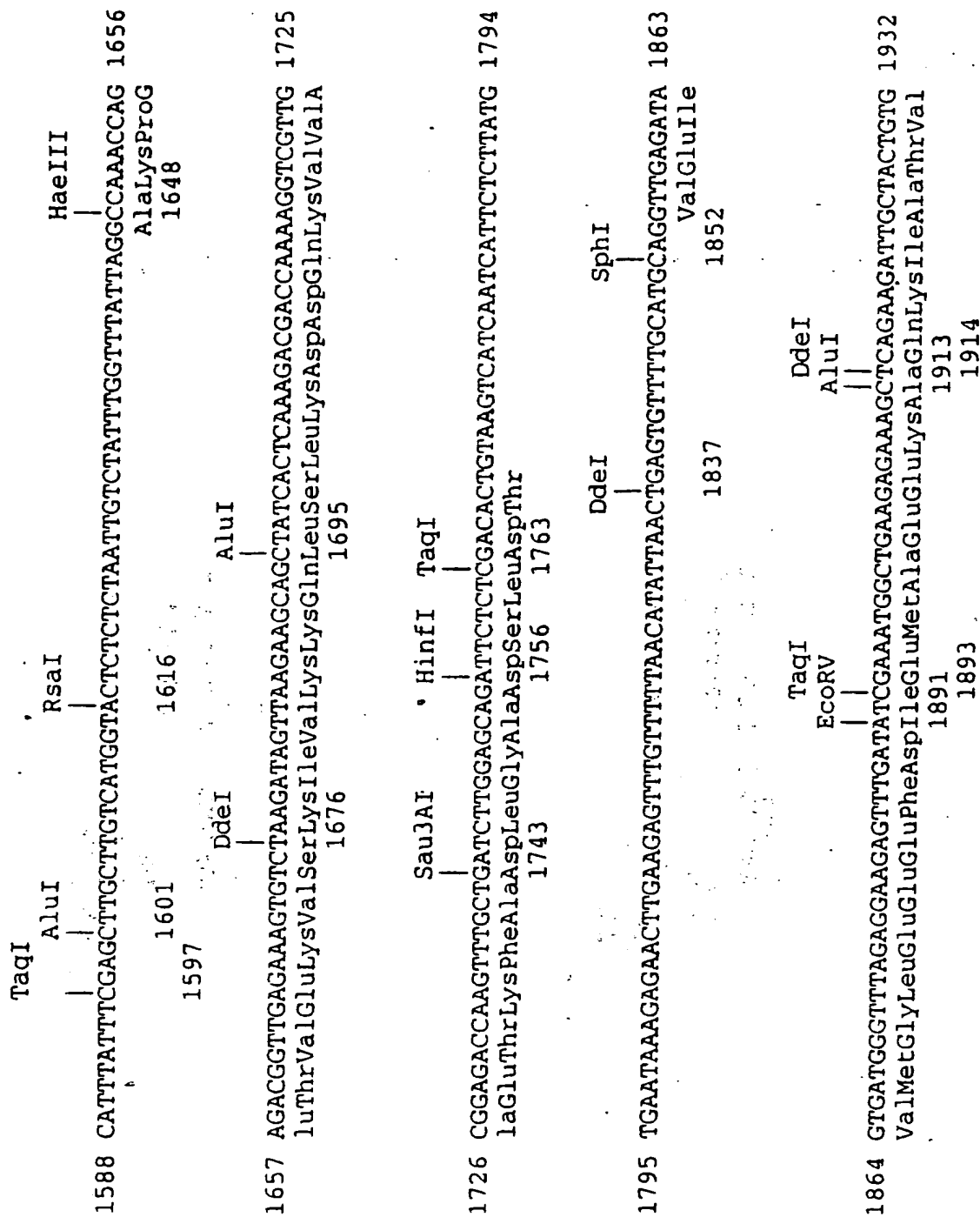


FIG. 3F

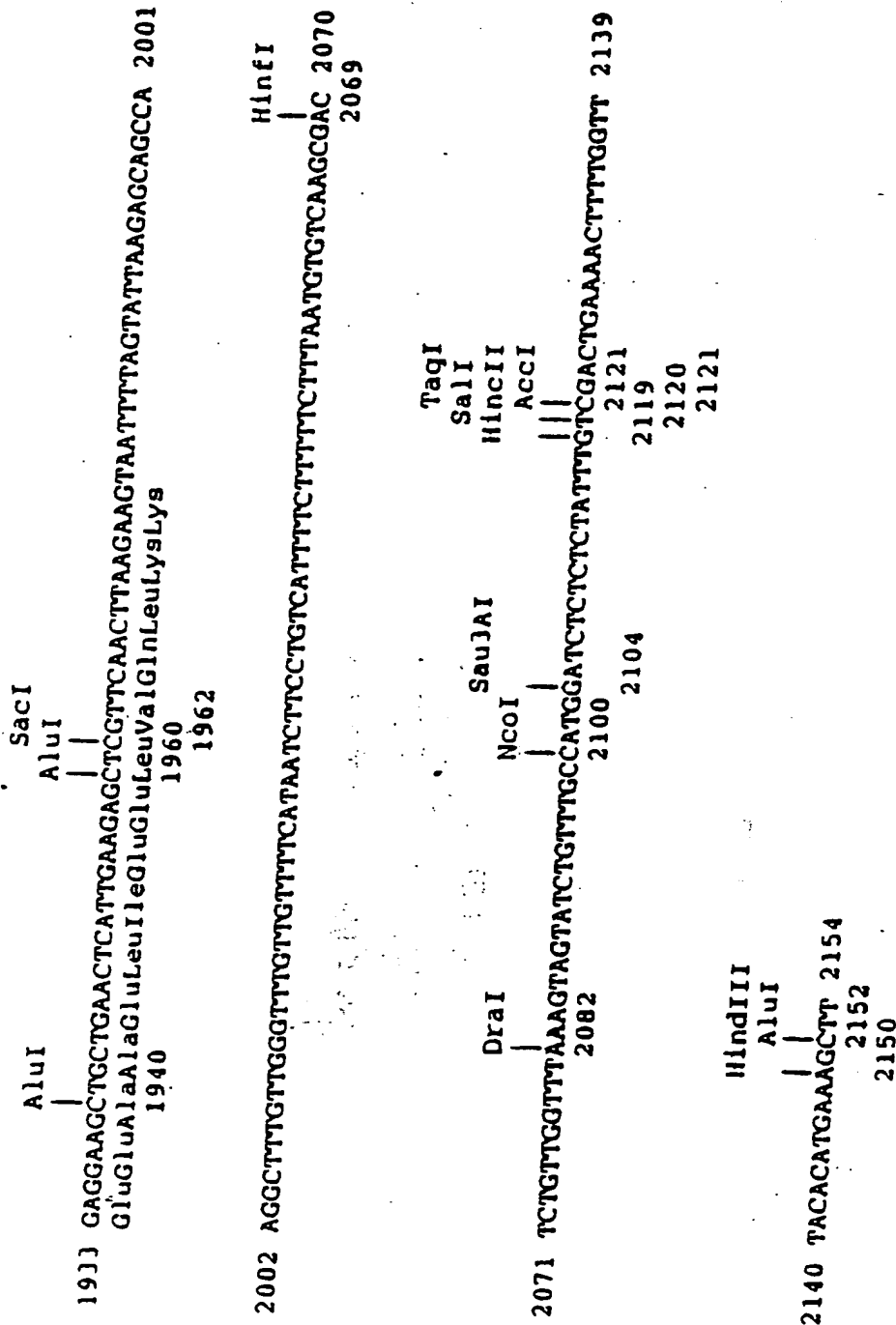
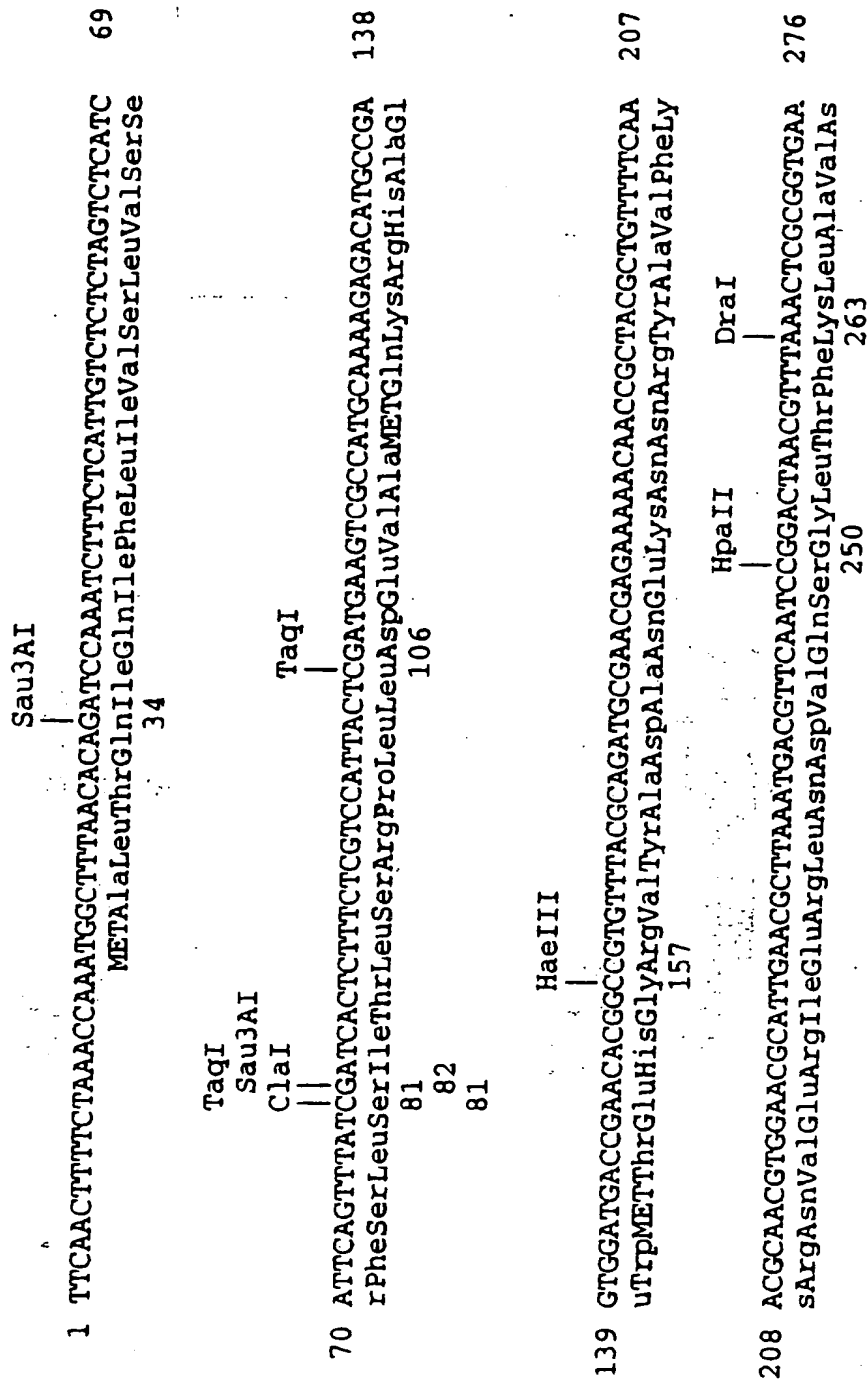


FIG. 3G

Brassica Campestris Seed Specific cDNA-EA9



Complete nucleotide sequence of *B. campestris* cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of the sequence and a potential polyadenylation signal is underlined.

FIG. 4A

345

277 CCAGTTTGCTGATCTAACCAACGAAGAATTCCGTTCTATGTACACTGGTTTCAAGGAAACTCTGTGTT
nGlnPheAlaAspLeuThrAsnGluGluPheArgSerMETTyrThrGlyPheLysGlyAsnSerValle
287 303 318

346 GTCTAGTCGAACCTAACCAACGTCGTTTAGGTACCAAAACGTTTCTTCTGATGCGTTGCCGGTTTCTGT
uSerSerArgThrLysProThrSerPheArgTyrGlnAsnValSerSerAspAlaLeuProValSerVa
353 380 405

378

414

415 TGATTGGAGGAAGGAGCTGTGACTCCTATCAAGGATCAAGGCTTATGCGGATCTTGTGGCGGTT
lAspTrpArgLysLysGlyAlaValThrProIleLysAspGlnGlyLeuCysGlySerCysTrpAlaPh
435 452 468

483

484 TTCAGCTGTTGCCGGCTATAGAAGCAGTAGCACAGATAAAGAAAGGAACTCATTTCTTTGTCTGAACA
eSerAlaValAlaAlaIleGluGlyValAlaGlnIleLysLysGlyLysLeuIleSerLeuSerGluGI
489 499

552

FIG. 4B

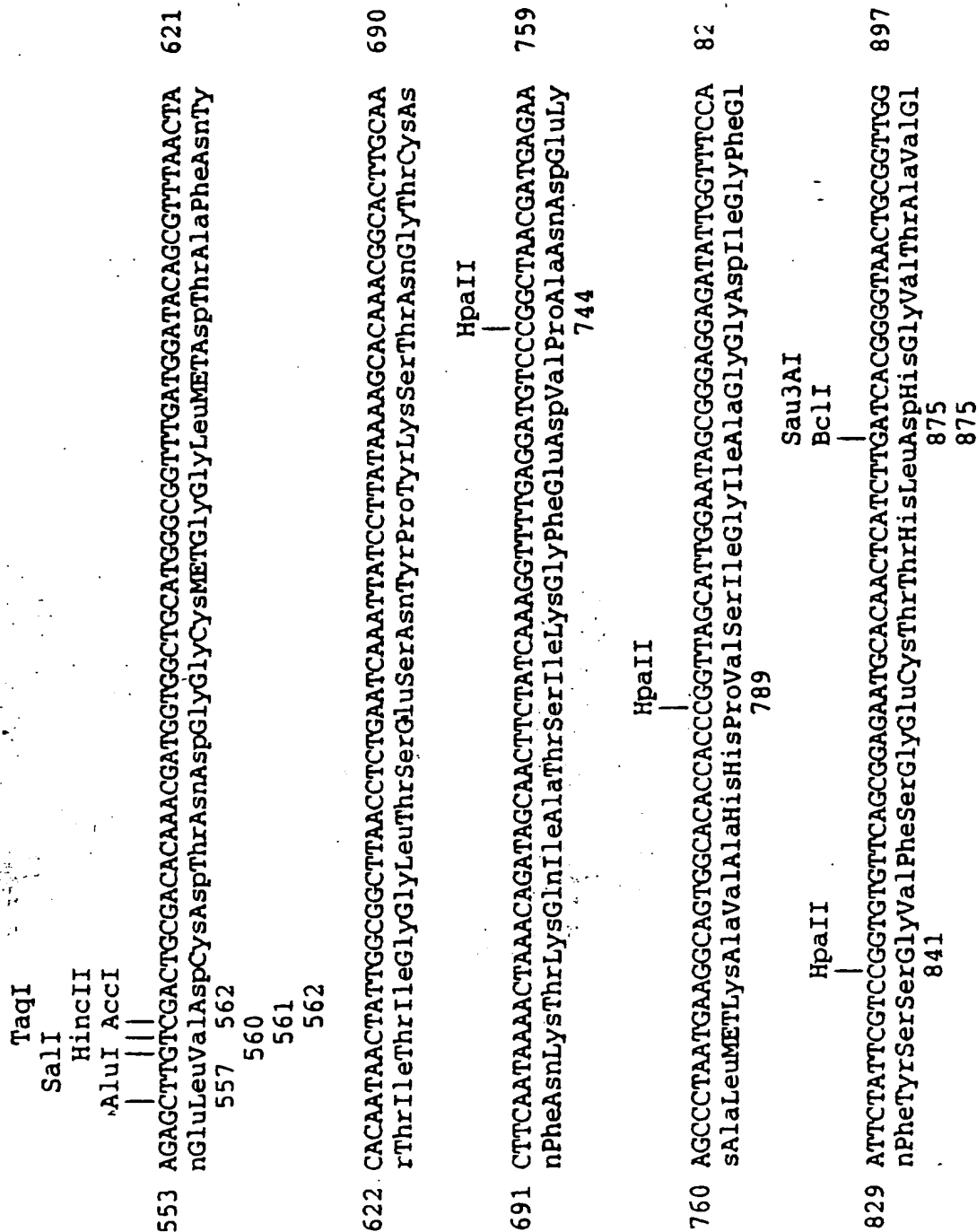


FIG. 4C

898 ATACGGCCGATCTAAACCGGATTAAAGTACTGGATCCTCAAGATTCATGGGACCAAAATGGGAGA 966
 yTyrGlyArgSerLysAsnGlyLeuLysTyrTrpIleLeuLysAsnSerTrpGlyProLysTrpGlyG1
 904 906 927 931 941 951
 Sau3AI HaeIII ScaI Sau3AI RsaI BamHI EcoRI AvaII

967 ACGTGATACATGAGGATCAAAAAAGATATCAAGCCTAAACACGGACAATGTGGTCTTGCCATGAATGC 1035
 uArgGlyTyrMETArgIleLysLysAspIleLysProLysHisGlyGlnCysGlyLeuAlaMETAsnAl
 982 995
 Sau3AI EcoRV

1036 TTCGTACCCAACTATGTGAAAAAATCGGTTCAATATCCGGTTAAGCTTTAGAAATAAATGTGTGTGTGG 1104
 aSerTyrProThrMET
 1041 1073 1081 1079
 RsaI HindIII HpaII AluI

1105 TTATAATTAAAGACTCTGTTCATGTAATTGTGAAATGGTAAGTTTATGTGATGCAAAAGATTGATA 1173
 1174 AAAAAAAAAAAAAA 1186

FIG. 4D

3H11 TTTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA 51

3H11 GCTTACAGCTGGGAGAACATTGTCTAACTCTTCTGAAATTTAAATGTTATC 102

3H11 CAGAATCCTTCATCATAAAATAATATCAAAATGCAAATCTATTTTTTCTAC 153

3H11 TCTTGTCTAGCTTCAACTTTCTTCTTCTGCTCATCAATTAGCAATTAATCC 204
TGCTCATCAATTAGCAATTAATCC

3H11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC 255
2A11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC
METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe

3H11 GTTGTTCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTCGAAAATG 306
2A11 GTTGTTCTTTTGACGACCACTTTAGTTGATATGTCTGGAATTCGAAAATG
ValValLeuLeuThrThrThrLeuValAspMETSerGlyIleSerLysMET

3H11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG 357
2A11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG
GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET

3H11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA 408
2A11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA
LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer

3H11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG 459
2A11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG
AsnSerAspCysIleGlyIleThrLeuCysGlnPheCysLysGluLysThr

3H11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCTTGAACAATA 510
2A11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCTTGAACAATA
AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro

FIGURE 5A

3H11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA 561
2A11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA

3H11 TAGTGTTGCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612
2A11 TAGTGTTGCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT

3H11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT 663
2A11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT

3H11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATTCCACATTAAT 714
2A11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATTCC

3H11 TCACGTATTTATTTCACTTATGATACGTATTTTGTTCCTTTCGCGTAAAA 765

3H11 AAAAAAAAAA 774

FIGURE 5B

2A11	①MALRDIPPQETLL
PA1b	①CSPFDIPPCGSPLCRCI
Chick pea inhibitor	①CT-KSIPP-----QCRCN
Lima bean inhibitor	LCT-KSIPP-----QCRCT
α_1 -antitrypsin	LGAIPMSIPPEV

2A11	TNILLGLCNEPCSSNSDCI
PA1b	GSPLCRCPAGLVIGNCR
Barley chloroform/ methanol-soluble protein d	TNLLGNCR-FYLVQQTCA
Wheat α -amylase inhibitor 0.28	VSALTGCR-AMVKLQ CV
Wheat albumin	VPALPACRPL-LRLQ-CN
Millet bi-functional inhibitor	NNPLDSCRWYVS _{AT} ER _{TC} CG
Castor bean 2S small subunit	QQNLRQCQEYIKQQVSGQ
Napin small subunit	AQNLRA _{CC} QQWLNKQAMQS

FIGURE 6

2A11 GENOM.

10	20	30	40	50
CTCGAGCCCT	TTAAAAAGTA	TAGTCAATAT	TTACGGTGAC	CGTGAATTTT
60	70	80	90	100
TTAATTATGA	TATATAATTT	AAAAGAAATC	ATGATCACAT	TCTACTGATG
110	120	130	140	150
AGAACATGTG	CTAATCAAGG	GAAAACATGG	ATGTGAAAAA	TACTTTTTGT
160	170	180	190	200
TAAAAGTAAA	AAAAAATGTG	AAATTTTGTG	AGTTATTTAC	TACCTATACA
210	220	230	240	250
TTATTTGAGC	ATGTGCAAAC	TTTACAAATA	CCTAATAGAA	GATTTTCACC
260	270	280	290	300
TGCCTGTATA	TATGTAAATT	AATTATAATG	AACACTCTCA	CATAAAATAA
310	320	330	340	350
TTATCAGTAT	ATACATTAAT	ACTTGCCCTC	CACAATGAAT	TAAATAAAAT
360	370	380	390	400
GTAGAACATG	ATCTACACTT	CAATAAAACT	AAGACCATAA	AGAATAATTT
410	420	430	440	450
CAAAATATAC	ACATGTCAAC	AATAAATTAT	TTGCATATTA	TATTAECTTA
460	470	480	490	500
CTAAACAATC	TTTACTTTTG	AAATATAAAA	ATAATCAAGT	TATAAGTCTG
510	520	530	540	550
CTCAAAGTAA	AGCACTTGTT	AGACTCATCT	GATTTTGAGA	AGGTAAGCAA
560	570	580	590	600
ATTGATGGTG	CATAATAGTC	ACAAGTAAAA	TATAAAATAG	ATTTTCATTAG
610	620	630	640	650
TAAAATTGTT	TTTTACTTTC	TTTATATATA	ATTATCAATA	TCCTTCAATG
660	670	680	690	700
GTAGGTTAAT	TATATTGTTA	ACTTCTTGTT	GAATTAAAGC	AATAAGACAA
710	720	730	740	750
GAATATTAAA	GATAAAAGAA	CAATAAAAAT	AGAAAGACTA	AGAGATAAGA
760	770	780	790	800
GTTTTCTTAT	TCTTCTTTCA	ATAAGTATCA	TCAAGTGTAT	ACAATATAAA
810	820	830	840	850
TTTTTGTTAT	TTTGATCTAT	CTATTTATAA	TGTTATATAT	AAGCATACAA
860	870	880	890	900
AAGATCAGTC	ATAAATATGA	CTTTAATCAT	GAAAATAATG	AAAGAGATTA
910	920	930	940	950
TGAAGGCGTA	AGGTTACTAG	AATAATAGTC	ATTAAAAAAA	GGGGTTATCT
960	970	980	990	1000
TTATAATTGA	ATAATTGATG	AAGTAATGGA	GATAATTAGT	GAGCATAAAT
1010	1020	1030	1040	1050
TTTTTTAAAA	AAATGGACAT	TTACACTATA	ATATTTTATA	ACACTTTCCC
1060	1070	1080	1090	1100
TTAAACATCT	AGGTATAAAT	AATGAGTCTT	GTCAAAATCT	TAGTAGGAAA

FIGURE 7A

1110	1120	1130	140	1150
AATTCTGTGA	AATTTTTTTA	GTGAAAACAA	ATGATATAAA	TATCTTGAAT
1160	1170	1180	1190	1200
ACTCATTATT	TGTTGTCTCA	TTAAAAATCT	TATCTGACCT	ATAAAAATAAA
1210	1220	1230	1240	1250
TTATTTGCTC	AACTCAAAAT	AGTTTTTCAT	TCTAAAATTA	GTATAATTAT
1260	1270	1280	1290	1300
TAGTGAATAT	TTAATTAACA	TAATTGTATA	CTAAGGGGCC	TATAAATTGG
1310	1320	1330	1340	1350
ATTCTTCTCA	AAGAAAAATA	AAATCACCAC	ACAACTTTCT	TCTTCTGCTC
1360	1370	1381	1390	
ATCAATTAGC	AATTAATCCA	AAACCATT	ATG GCT GCC AAA AAT	
			MET Ala Ala Lys Asn	
1399	1408	1417	1426	
TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT GTT CTT TTG				
Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val Leu Leu				
1435	1444	1454	1464	1474
ACG ACC ACT TTA GGTTCAAC	ACTTCTCCCT	TATTTTGTTT		
Thr Thr Thr Leu				
1484	1494	1504	1514	1524
TCTTAATTC	TTGGAAGTCA	TATGCATGTG	TTTGGTATCA	TGGTATATAT
1534	1544	1554	1564	1574
ATAAAGGAAA	ATATTTTCT	TAATTACTGG	TTTTCTAATG	TTTGGTAGGT
1584	1594	1604	1614	1624
AATCGGAAAT	TATTATGAGA	TAATGAACCT	GCAAAGTCAT	TATTATATAA
1634	1644	1654	1664	1674
CTTTTTTTTT	ATACTTTGAT	TTAAGAATTC	ATTTTTCTCA	TTTTATATAA
1684	1694	1704	1714	1724
ACTTATTTTT	CAACAGAAAA	TATTTTTTCGA	ACTATTCAAA	CACACCCTAA
1734	1744	1754	1764	1774
GACATTACAT	ATATATATAT	ATACAGGCTG	CGTTTTATAT	TACTTAATGC
1784	1794	1804	1814	1824
CTATTGAGTT	GGCCCACCCT	TTAAGAATGA	TTCAATTAGA	GATATGTTTT
1834	1844	1854	1864	1874
ACTAAATTAA	CCTATGCTTT	AAGACTCTAA	ATTTGGCTAT	TACTATTTTA
1884	1894	1904	1914	1924
CGTTGTAATT	TAATGACAAA	CATTTCATAA	TGACTATAGT	CTGAACTTAA
1934	1944	1954	1964	1974
TTAGACAGAC	GTATCTATAG	TTTGCTTACT	AATGATTCAT	AGCTATATAT
1984	1994	2004	2014	2024
TTGGAGAGGA	GAGAGACAAA	CGATATTAAG	AAAGGGAGGA	GAGAGGCGAG
2034	2044	2054	2064	2074
GTAAATCTGA	AATAGAGAAG	AGAAAGGCAA	CCAATTTTGA	TCATCTATCA
2084	2094	2104	2114	2124
TACTTTTGAT	TATTATTTTT	ATTATATGTA	CGTTTACATT	ACAGTTTTTCG

FIGURE 7B

2134	2144	2154	2164
AATTCTTACA TTAATCTTAA TCATAATATA TACA GTT GAT ATG			
			Val Asp MET
2173	2182	2191	2200
TCT GGA ATT TCG AAA ATG CAA GTG ATG GCT CTT CGA GAC			
Ser Gly Ile Ser Lys MET Gln Val MET Ala Leu Arg Asp			
2209	2218	2227	2236
ATA CCC CCA CAA GAA ACA TTG CTG AAA ATG AAG CTA CTT			
Ile Pro Pro Gln Glu Thr Leu Leu Lys MET Lys Leu Leu			
2254	2263	2272	2281
CCC ACA AAT ATT TTG GGA CTT TGT AAC GAA CCT TGC AGC			
Pro Thr Asn Ile Leu Gly Leu Cys Asn Glu Pro Cys Ser			
2290	2299	2308	2317
TCA AAC TCT GAT TGC ATC GGA ATT ACC CTT TGC CAA TTT			
Ser Asn Ser Asp Cys Ile Gly Ile Thr Leu Cys Gln Phe			
2326	2335	2344	2353
TGT AAG GAG AAG ACG GAC CAG TAT GGT TTA ACA TAC CGT			
Cys Lys Glu Lys Thr Asp Gln Tyr Gly Leu Thr Tyr Arg			
2371	2380	2393	2403
ACA TGC AAC CTG TTG CCT TGA ACAATATCAA TGATCTATCG			
Thr Cys Asn Leu Leu Pro			
2413	2423	2433	2443
ATCGATCTAT CTATCTATTT ATCTGTCTCT GCGCGTATAG TGTTGTCTGT			
2463	2473	2483	2493
ACCTTTGGTG TGAAGAATAT GAATAAAGGG ATACATATAT CTAGATATAT			
2513	2523	2533	2543
TCTAGGTAAT GTCCTATTGT ATTTAAAATT TGTAGCAATG ATTGTTTGAA			
2563	2573	2583	2593
TAAAAACATA CCATGAGTGA AATAATTATT CCACATTAAAT TCACGTATTT			
2613	2623	2633	2643
ATTTCACTTA TGATACGTAT TTTTGTTCCT TTCGCGTAGA TTTTGTATCC			
2663	2673	2683	2693
TTTTCCCTTT TGAATATTAA ACATTAAACA CAAATAATGT TTATTAAATT			
2713	2723	2733	2743
AAGTTAATAT TTTTATTTAG CTATTTATAT TTTTATTTGA AATCAAACCTT			
2763	2773	2783	2793
GATAAATATT TATAAAGATA ATTAACAAGT AATGTGACAC TAACACCATG			
2813	2823	2833	2843
TAATATTATC TTGTCGTTAT TTATGATAAT ATTTTAAAAT TATAATTTC			
2863	2873	2883	2893
GTTAAAAAAT TATTAAAAAA ACATACTTTT AAAAAGTGAG TTAGCCTCCG			
2913	2923	2933	2943
CTACCCACAT ACTTATGAAT TGGACTAGTT GTTTTTTTGAC CCACAAAAAG			
2963	2973	2983	2993
AATGGGCTAA TTAAACCTGA CCTATCAAAT TTCAGAATCT GCATAGATTA			

FIGURE 7C

3013	3023	3033	3043	3053
GTCCGAACGA	AATGAGTCAG	CCCGTATTGA	ACAAAATATC	AACAAGGACG
3063	3073	3083	3093	3103
TTATGTAAAG	ATGTTTAAGA	AGGAAAAAAG	ATTTCTAATA	CATATGGACT
3113	3123	3133	3143	3153
TTCAATATCC	CAACTTTGTC	TGGCGATCTG	AACCCTGCTT	AGTTTGTGTA
3163	3173	3183	3193	3203
TCATTAACCT	GTCTTGCTAT	GTATTTAAGA	TTTAAACTTT	ATATGTTTAA
3213	3223	3233	3243	3253
ACTTACAGAA	AATACATATA	AATCTCTCAA	GACTTGCGAA	CATAATTTAC
3263	3273	3283	3293	3303
TTTAGTACTT	AAACTACATG	AAAATTTAAA	TATCCTTTTA	ACATCTTTGA
3313	3323	3333	3343	3353
AGTGAATTAA	ATTATCACAA	TCCGAGCCTA	CACCTTGGAC	GTGGCCGGCA
3363	3373	3383	3393	3403
CTCAAGAACC	AGTGCTGGTC	CCCAAGCTAA	CCCTCATCCT	GACTGACTAC
3413	3423	3433	3443	3453
AAGCGGAAGG	CTAACTTAAG	TATACAAAAG	CTTAAACTTG	AATAAAATAA
3463	3473	3483	3493	3503
ACTTTACAAG	GTTTTAACAC	AAATGAACAA	CTTTGAAGAA	AATAATATAT
3513	3523	3533	3543	3553
TCAACTAGCC	ATAAAATAGA	CAACTTTAGT	CTTTAAAACA	TTTAATAAAA
3563	3573	3583	3593	3603
TAAATGCAAA	ATATAGACTC	CTTAACTAAA	CTGACTATCT	ATGGAGCCTC
3613	3623	3633	3643	3653
TAATTGATAA	AGATGGAAGT	CGGGACAAGA	CCACGAGATC	CTGACTAAAC
3663	3673	3683	3693	3703
TGAGAAGTAA	ATAAAATCCC	CCGGAAAAAA	AGGAGCCTCA	CCATGGCTAA
3713	3723	3733	3743	3753
CTCGAACTCG	GGGATATATC	AATGAAGCTC	CTGTTGATGA	TCTTGAAGAC
3763	3773	3783	3793	3803
ATGTCTCTGC	ATCATCAAAA	AGATGCAGGC	CAAATGGCTC	AGTACGTAAA
3813	3823	3833	3843	3853
ATGTACGAGT	ATGTAAGGGA	AATTCTAAAG	TATAACATAA	GCTTGATACT
3863	3873	3883	3893	3903
TGAATAAAAAG	GAAACATACT	TACCTCTTTT	CAACTCAACT	CAAATTAAGA
3913	3923	3933	3943	3953
ATAAGATACT	CAACTCAAAG	ATTAGGTATT	CAACGCAAAT	ATGGCACTCT
3963	3973	3983	3993	4003
ACTCAATGAA	GTACAAATTA	ACTCAGGATA	CTCGACTTAA	GATACTCAAC
4013	4023	4033	4043	4053
TCCCGACACT	CAACTGAACT	CATTTCAATA	TAAAGCAGCT	TAAAACAAGT
4063	4073	4083	4093	4103
TCAGTATAAA	GTAAAGTTGT	TTAAAAACAT	GATGTCAACT	CTGTGTGTAT
4113	4123	4133	4143	4153
AATAAGGGAT	ACAACATAAC	TTTGAAATGT	ATATAAAAAT	ACAATTAACT

FIGURE 7D

416	4173	4183	4193	4203
GATGTATATA	AAAATACATT	AATCTATGGG	AGATTCTCTA	ACCGACAACC
4213	4223	4233	4243	4253
ATCACTTAAG	GGCTAAGATG	ATGATATAGC	GATCTACCGC	ACGCTGCCAT
4263	4273	4283	4293	4303
CGCATCTTAT	ACCCGGCCAA	AGGTATAAGA	CCTGAACTGC	CTAATGAATC
4313	4323	4333	4343	4353
CACTAATAAA	CTGTTAAAAG	GAATCATCTA	AAAAGTATGA	CCCTTTTCTA
4363	4373	4383	4393	4403
CCCATAGTGG	CTAACATGGT	TTATGGGGGC	TGTGAGTTAT	CTGAACTCTC
4413	4423	4433	4443	4453
CCCCATATCG	GTGCTCAATA	CTACTCCAAA	AAATATACTG	CTCTTATGTT
4463	4473	4483	4493	4503
TAAAAACATA	CTGATTCTGT	GGTTTGAAAT	TATTGCTTAA	AGCTTAGATT
4513	4523	4533	4543	4553
TTTGAAAAGC	TCTCTTTTGA	AAATCGTAGT	TTCCTTTTTC	TTCTATTAAA
4563	4573	4583	4593	4603
GCTAGACATA	GGCTATGTAG	AACTCTAGCT	TACCTTCCTT	CTCAAAAGTT
4613	4623	4633	4643	4653
TGAAAACATT	TGCTTAGATT	CTTAGGGACT	ACTTAGTTCC	CTTGTTGGAA
TTC				

FIGURE 7E

PG GENOMIC

10	20	30	40	50
AAGCTTCTTA	AAAAGGCAAA	TTGATTAATT	TGAAGTCAAA	ATAATTAATT
60	70	80	90	100
ATAACAGTGG	TAAAGCACCT	TAAGAAACCA	TAGTTTGAAA	GGTTACCAAT
110	120	130	140	150
GCGCTATATA	TTAATCAACT	TGATAATATA	AAAAAAATTT	CAATTCGAAA
160	170	180	190	200
AGGGCCTAAA	ATATTCTCAA	AGTATTCGAA	ATGGTACAAA	ACTACCATCC
210	220	230	240	250
GTCCACCTAT	TGACTCCAAA	ATAAAATTAT	TATCCACCTT	TGAGTTTAAA
260	270	280	290	300
ATTGACTACT	TATATAACAA	TTCTAAATTT	AAACTATTTT	AATACTTTTA
310	320	330	340	350
AAAATACATG	GCGTTCAAAT	ATTTAATATA	ATTTAATTTA	TGAATATCAT
360	370	380	390	400
TTATAAACCA	ACCAACTACC	AACTCATTA	TCATTAAATC	CCACCCAAAT
410	420	430	440	450
TCTACTATCA	AAATTGTCCT	AAACACTACT	AAAACAAGAC	GAAATTGTTC
460	470	480	490	500
GAGTCCGAAT	CGAAGCACCA	ATCTAATTTA	GGTTGAGCCG	CATATTTAGG
510	520	530	540	550
AGGACACTTT	CAATAGTATT	TTTTTCAAGC	ATGAATTTGA	AATTTAAGAT
560	570	580	590	600
TAATGGTAAA	GAAGTAGTAC	ATCCCGAATT	AATTCATGCC	TTTTTTAAAT
610	620	630	640	650
ATAATTATAT	AAATATTTAT	GATTTGTTTT	AAATATTAAA	ACTTGAATAT
660	670	680	690	700
ATTATTTTTT	TAAAAATTAT	CTATTAAGTA	CCATCACATA	ATTGAGACGA
710	720	730	740	750
AGGAATAATT	AAGATGAACA	TAGTGTTTAA	TTAGTAATGG	ATGGGTTAGTA

FIGURE 8A

760	770	780	790	800
AATTTATTTA	TAAATTATAT	CAATAAGTTA	AATTATAACA	AATATTTGAG
810	820	830	840	850
CGCCATGTAT	TTTAAAAAAT	ATTAAATAGT	TTGAATTTAA	AACCGTTAGA
860	870	880	890	900
TAAATGGTCA	ATTTTGAACC	CAAAAGTGGA	TGAGAAGGGT	ATTTTAGAGC
910	920	930	940	950
CAATAGGRGG	ATGAGAAGGA	TATTTTGAAG	CCAATATGTG	ATGGATGAAG
960	970	980	990	1000
GATAATTTTG	TATCATTTCT	AATACTTTAA	AGATATTTTA	GGTCATTTTC
1010	1020	1030	1040	1050
CCTTCTTTAG	TTTATAGACT	ATAGTGTTAG	TTCATCGAAT	ATCATCTATT
1060	1070	1080	1090	1100
ATTTCCTGCT	TAAATTATTT	TTTATTTTAT	AAATTTTTTA	AAAATAAATT
1110	1120	1130	1140	1150
ATTTTTTCCA	TTTAACTTTG	ATTGTAATTA	ATTTTTTAAA	ATTACCAACA
1160	1170	1180	1190	1200
TATAAATAAA	ATTAATATTT	AACAAAGAAT	TGTAACATAA	TATTTTTTTA
1210	1220	1230	1240	1250
ATTATTCAAA	ATAAATATTT	TTAAACATCA	TATAAAAGAA	ATACGACAAA
1260	1270	1280	1290	1300
AAAATTGAGA	CGGGAGAAGA	CAAGCCAGAC	AAAAATGTCC	AAGAAACTCT
1310	1320	1330	1340	1350
TTCGTCTAAA	TATCTCTCAT	CCAAACTAAT	ATAATACCCA	TTATAATTAA
1360	1370	1380	1390	1400
CCATATTGAC	CAACTCAAAC	CCCTTAAAAT	CTATAAATAG	ACAAACCCTT
1410	1420	1430	1440	1450
CCCATACCTC	TTATCATAAA	AAAAATAATA	ATCTTTTTCA	ATAGACAAGT
1460	1470	1480	1490	1500
TTAAAAACCA	TACCATATAA	CAATATATCA	TGGTTATCCA	AAGGAATAGT

FIGURE 8B

1510	1520	1530	1540	1550
ATTCTCCTTC	TCATTATTAT	TTTTGCTTCA	TCAATTTCAA	CTTGTAGAAG
1560	1570	1580	1590	1600
CAATGTTATT	GATGACAATT	TATTCAAACA	AGTTTATGAT	AATATTCTTG
1610	1620	1630	1640	1650
AACAAGAATT	TGCTCATGAT	TTTCAAGCTT	ATCTTTCTTA	TTTGAGCAAA
1660	1670	1680	1690	1700
AATATTGAAA	GCAACAATAA	TATTGACAAG	GTTGATAAAA	ATGGGATTAA
1710	1720	1730	1740	1750
AGTGATTAAT	GTACTIONAGCT	TTGGAGCTAA	GGGTGATGGA	AAAACATATG
1760	1770	1780	1790	1800
ATAATATTGT	AAGTATTTAA	ATATTGGAAT	ATATTTGTGG	GGATGAAAAT
1810	1820	1830	1840	1850
GATAGAGAAT	ATAAGAATTA	TTTGAAGGA	TGAAAAGTTA	TATTTTATAA
1860	1870	1880	1890	1900
AGTAGAAAAT	TATTTTCTCG	TTTTTAGTAA	TTAAAGGTGA	AAAATGAGTT
1910	1920	1930	1940	1950
TTCTCGTAAG	CGAGGAAAGT	CATTTTCCAT	GGAAGTGTAT	TTTTTTTTTA
1960	1970	1980	1990	2000
CTTTTAATAA	CGTCATAGTA	TTTGCTATAC	TCAAGAATAA	GACACTATTA
2010	2020	2030	2040	2050
TTGATGTTTA	GTGCTCGAAA	AGAAATTGAT	AGTAATTTTG	CTAATATAAC
2060	2070	2080	2090	2100
TATCAATTTT	TTATATGTAT	ATTTTTC AAC	CAAAATAACA	AAGCGTAATC
2110	2120	2130	2140	2150
CAATAAGTGG	GCCTCTAGAA	TAAAGAGTAA	GTTCTATTAA	TTCTTAACCT
2160	2170	2180	2190	2200
TATTTAATTT	TATGGAAACC	TCGACAAAAC	GACAATGCTC	AACTTATATT

CGAATTC

FIGURE 8C

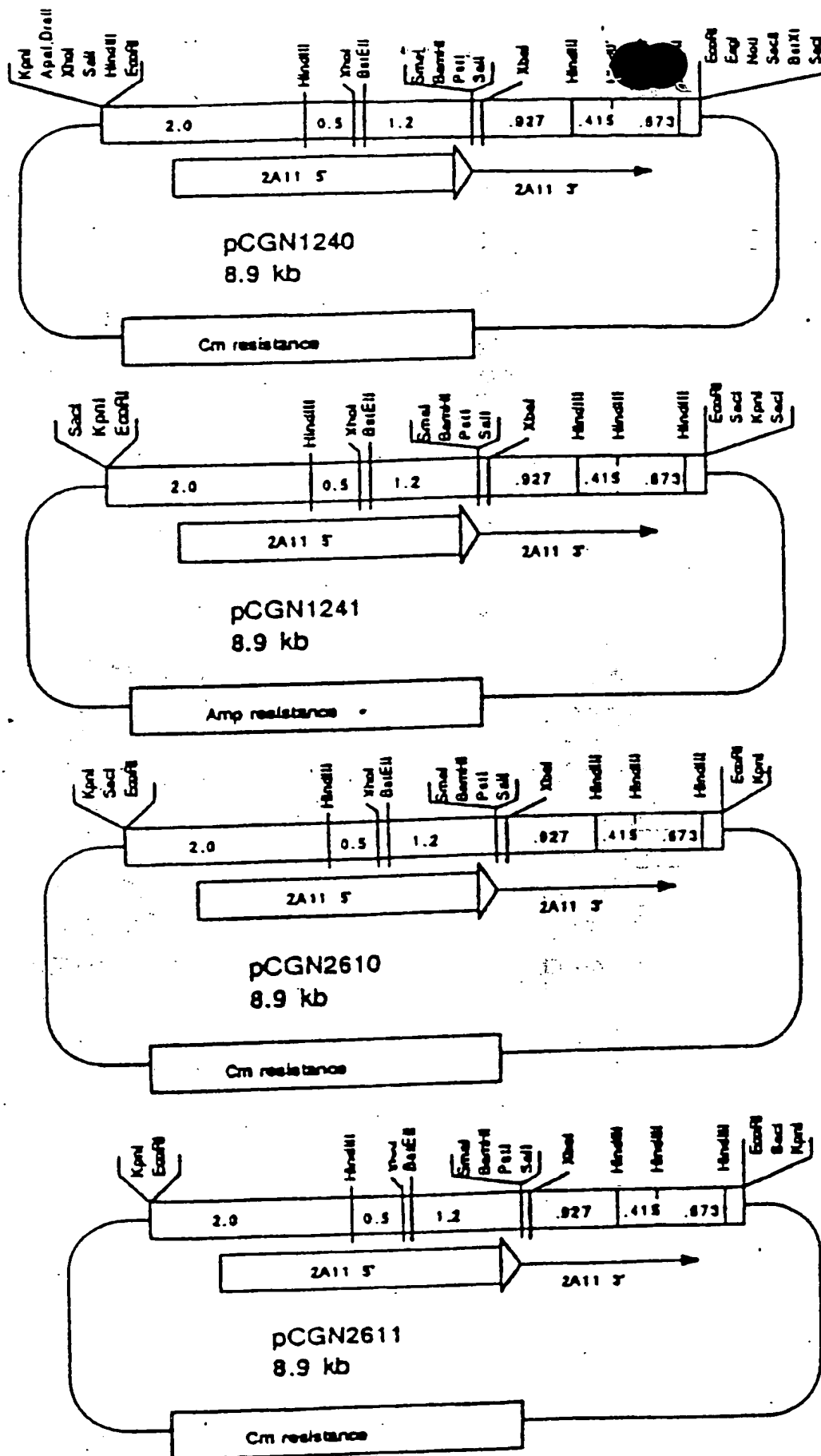


FIGURE 10